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Fax Cover Sheet

Date: 28 Sep 2004

5 Pgs

To: Dr. Stuart Macphail	From: Maher M. Haddad
Application/Control Number: 09/787,097	Art Unit: 1644
Fax No.: (617) 542-8906 212-258-2291	Phone No.: (571) 272-0845
Voice No.: 212-641-2215	Return Fax No.: (703) 273-0845
Re:	CC:
<input type="checkbox"/> Urgent <input type="checkbox"/> For Review <input type="checkbox"/> For Comment <input type="checkbox"/> For Reply <input checked="" type="checkbox"/> Per Your Request	

Comments:

Stuart,

Enclosed please find a couple of references that would read on the nucleic acid comprising a sequence encoding a fusion protein comprising the antigenic fragment and a heterologous sequence. Adams et al teaches a 396 nucleic acid sequence that encodes 86 amino acid seq of SEQ ID NO: 12 and a heterologous sequence. Also, Bonaldo et al teaches a 435 nucleic acid sequence comprising a sequence encoding a fusion protein comprising a fragment of a 76 amino acid in length and a heterologous sequence. The prior art reads on claims 6, 47, 48 and 60-65.

Maher Haddad

Maher Haddad

Number of pages __ including this page

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163 GlucyGlnProAsnArgIleMetArgLeuArgPheAsnHisPheAlaThrGluCysSer 182
165 GAAGGACGAGCAATGAAATGAGACTTCGCTTCAACATTTTCTACAGATGATGAC 224
183 TtpAspHisLeuTyrValTyrAspGlyAspSerIleTyrAlaProLeu 198
225 TGGGACCATTTATATGTTTATGATGGGACTCAATCTAGCACTCTG 272

AW120845 435 bp mRNA linear EST 22-OCT-1999
UI-M-BH2.3-aca-e-06-0-UI.s1 NIH BMAP M.S3.3 Mus musculus cDNA clone
UI-M-BH2.3-aca-e-06-0-UI 3', mRNA sequence.
AW120845
AW120845.1 GI:6096178
EST.
Mus musculus (house mouse)

US-09-787-097-12 (1-1429) x AW120845 (1-435)
QY 123 GlyTyrValGlyGluGlnCysGlnHisCysGlyArgPheArgLeuThrGlySerSer 142
Db 44 GCGTGGGTGGGCGAGCAATGCGACCTGCGGGCGCGCTTCAGACTAACTGGCTCTCT 103
QY 143 GlyPheValThrAspGlyProGlyAsnTyrIlystTyrIlystTyrIlystTyrIlyst 162
Db 104 GATTTGTAAACAGATGGACCTGGGAAATTATAATATAAGACGAGTGCATGGCTCAIT 163
QY 163 GluGlyGlnProAsnArgIleMetArgLeuArgPheAsnHisPheAlaThrGluCysSer 182
Db 164 GAAGGACGAGCAATGAAATGAGACTTCGCTTCAACATTTTCTACAGATGATGAC 223
QY 183 TtpAspHisLeuTyrValTyrAspGlyAspSerIleTyrAlaProLeu 198
Db 224 TGGGACCATTTATATGTTTATGATGGGACTCAATCTAGCACTCTG 271

RESULT 62
BI202684
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
COMMENT

435 bp mRNA linear EST 29-APR-2002
UI-M-CG0p-brk-h-05-0-UI.s1 NIH BMAP Ret4 S2 Mus musculus cDNA clone
UI-M-CG0p-brk-h-05-0-UI 3', mRNA sequence.
BI202684
BI202684.1 GI:14668656
EST.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 435)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
discovery
Genome Res. 6 (9), 791-806 (1996)
97044477
8889548
Contact: Chin, H
National Institute of Mental Health
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
20892-9643, USA
Tel: 301 443 1706
Fax: 301 443 9890
Email: mEST@mail.nih.gov

Location/Qualifiers
1. .435
/organism="Mus musculus"
/mol type="mRNA"
/strain="C57BL/6J"
/db xref="taxon:10090"
/clone="UI-M-BH2.3-aca-e-06-0-UI"
/dev stage="27-32 days"
/lab host="DH10B (Life Technologies)"
/clone lib="NIH BMAP M.S3.3"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not 1; Site 2: Eco RI; The
NIH BMAP M.S3.3 library is a subtracted library of a
series, ultimately derived from a mixture of individually
tagged normalized libraries from ten regions of the mouse
brain (cerebellum, brain stems, olfactory bulbs,
hypothalamus, cortex, amygdala, basal ganglia, pineal
gland, striatum, hippocampus) after a series of
subtractions to reduce the representation of cDNAs from
which ESTs had already been generated. The following
serially subtracted libraries were generated in this
process: NIH BMAP M.S3.3, NIH BMAP M.S2, NIH BMAP M.S1.
The subtracted library (NIH BMAP M.S3.3) was constructed
as follows: PCR amplified cDNA inserts from NIH BMAP M.S2
clones from which 3' ESTs had been derived was used as a
driver in a hybridization with the NIH BMAP M.S2 library
in the form of single-stranded circles. The remaining
single-stranded circles (subtracted library) was purified
by hydroxyapatite column chromatography, converted to
double-stranded circles and electroporated into DH10B
bacteria (Life Technologies) to generate the

FEATURES
source
1. .435
Location/Qualifiers

ORIGIN
Alignment Scores:
Pred. No.: 435
Score: 76.00 Matches: 76
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.32% Indels: 0
DB: 10 Gaps: 0

NIH BMAP M.S3.3 library. This procedure has been
previously described (Bonaldo, Lennon and Soares, Genome
Research 6:791-806, 1996)
TAG_TISSUE=hypothalamus
TAG_LIB=NIH BMAP M.S3.3
TAG_SEQ=CGGTA

FEATURES
source
1. .435
Location/Qualifiers

Pred. No.: 5.98e-62 Length: 281
 Score: 89.00 Matches: 89
 Percent Similarity: 100.00% Conservatives: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 6.23% Indels: 0
 DB: 10 Gaps: 0

US-09-787-097-12 (1-1429) x BG015062 (1-281)

QY 588 SerAspPheMetAlaTyrAspIleAlaCysAspArgTyrSerValLeuProArgProAsp 607
 DB 279 TCAGATTTCATGGCTATGACATTCCTCTCAGCGCTGGTCAAGTCTCCAGACCTGAT 220
 QY 608 LeuHisHisAspValAsnArgPheGlyHisSerIleValLeuHisSerThrMetTyr 627
 DB 219 CTCACCATGATGCAACAGATTTGGCATTCACAGCATCTTACACACAGCACCATGTAT 160
 QY 628 ValPheGlyGlyPheAsnSerLeuLeuSerAspIleLeuValPheThrSerGluGln 647
 DB 159 GGTTCGGTGGTTCATAGTCTCTCTCAGCGACATCTGGTATTCACCTCGGAACAG 100
 QY 648 CysAspAlaHisArgSerGluAlaAlaCysLeuAlaIleArgProGlyIleArgCysVal 567
 DB 99 TGTGATGGCATCGAGAGGAGCGCTGTATTAGCAGCAGACCTGGTATTGGGTGTG 40
 QY 668 TrpAsnThrGlySerSerGlnCysIle 676
 DB 39 TGGACACACAGCGTCTCTCACTGTATC 13

RESULT 51

BF853021/c 483 bp mRNA linear EST 16-JAN-2001
 LOCUS BF853021-191200-001-g05 EN0093 Homo sapiens cDNA, mRNA sequence.

DEFINITION

MR2-EN0093

ACCESSION

BF853021

VERSION

BF853021.1 GI:12240869

KEYWORDS

EST

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

REFERENCE

1 (bases 1 to 483)

AUTHORS

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.

TITLE

Shotgun sequencing of the human transcriptome with ORF expressed

JOURNAL

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

MEDLINE

20202663

PUBMED

10737800

COMMENT

Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the PAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=MR2&t2=MR2-EN0093-191200-001-g05&t3=2000-12-19&t4=1)
 Seq primer: puc 18 forward
 High quality sequence stop: 483.

FEATURES

Location/Qualifiers

1..483

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/dev_stage="Adult"

/clone_lib="EN0093"

source

/notes="Organ: lung normal; Vector: puc18; Site: 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN

Alignment Scores:

Pred. No.: 1.02e-61 Length: 483
 Score: 89.00 Matches: 89
 Percent Similarity: 100.00% Conservatives: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 6.23% Indels: 0
 DB: 10 Gaps: 0

US-09-787-097-12 (1-1429) x BF853021 (1-483)

QY 1141 GluValGluLeuArgTyrGlnGlyAsnProLeuArgGlyThrCysTyrTyrThrLeuLeu 1160
 DB 446 GAGTAGAATCGATACCAAGGAACCTCTCAGAGGAACATGTTATTATCTCTCTT 387
 QY 1161 IleAspTyrGlnPheThrPheSerLeuSerGlnGluAspArgTyrTyrThrAlaIle 1180
 DB 386 ATTGACTATCAGTTCACCTTTAGTCTATCCAGGAAGATGCGCTATTACACAGCTATC 327
 QY 1181 AsnPheValAlaThrProAspGluGlnAsnArgAspLeuAspMetPheIleAsnAlaSer 1200
 DB 326 AATTTGTGCTACTCTCTGACGAACAACAGGATTTGCAATTCATCAATGCTCTC 267
 QY 1201 LysAsnPheAsnLeuAsnIleThrTrpAlaAlaSerPheSerAlaGlyThrGlnAlaGly 1220
 DB 266 AAGAATTTCAACTCAACATCACCTGGGCTGCCAGTTTCTCAGCTGGAACCCAGGCTGA 207
 QY 1221 GluGluMetProValValSerLysThr 1229
 DB 206 GAAGAGATGCTGTGTTCATCAAAACC 180

RESULT 52

AA350292

LOCUS

AA350292 396 bp mRNA linear EST 21-APR-1997

DEFINITION

EST57511 Infant brain Homo sapiens cDNA 3' end, mRNA sequence.

ACCESSION

AA350292

VERSION

AA350292.1 GI:2002619

KEYWORDS

EST

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

REFERENCE

1 (bases 1 to 396)

AUTHORS

Adams, M.D., Kerlavage, A.R., Fields, C. and Venter, J.C.

TITLE

3,400 expressed sequence tags identify diversity of transcripts from human brain

JOURNAL

Nat. Genet. 4, 256-267 (1993)

MEDLINE

93364420

PUBMED

8358434

COMMENT

Other ESTs: EST57512, THCI68885

Contact: Kerlavage, AR

Bioinformatics

The Institute for Genomic Research

9712 Medical Center Drive, Rockville, MD 20850 USA

Tel: 3018699056

Fax: 3018699423

Email: arkerlav@tigr.org

For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (http://www.tigr.org/cdb/hgi/hgi.html)

Seq primer: M13-21.

Location/Qualifiers

1..396

/organism="Homo sapiens"

/mol_type="mRNA"

source

/db_xref="ATCC (inhost):151062"
 /db_xref="taxon:9606"
 /sex="female"
 /dev_stage="infant"
 /clone_lib="infant brain"
 /note="Organ: brain; Vector: lafmid BA; Site_1: HindIII;
 Site_2: NotI"

ORIGIN

Alignment Scores:

Pred. No.: 2,26e-59 Length: 396
 Score: 86.00 Matches: 123
 Percent Similarity: 98.40% Conservatives: 0
 Best Local Similarity: 98.40% Mismatches: 1
 Query Match: 6.02% Indels: 2
 DB: 9 Gaps: 0

US-09-787-097-12 (1-1429) x AA350292 (1-396)

QY 480 TyrAspLeuAplYsAsnThrTrpSerIleLeuHisThrGlnGlyAlaLeuValGlnGly 499
 Db 1 TATGATTGGATAGAACACACTGGAGTATATTACACCCAGGGTCCCTTGTGCAAGG 60
 QY 500 GlyTyrGlyHisSerSerValTyrAspHisArgThrArgAlaLeuTyrValHis-GlyG 519
 Db 61 GGTACGGCCCATACGACGTGTTACGACCATAGGACAGGGCCCTATACGTTNA-TGGTGG 119
 QY 519 YTyLysAlaPheSerAlaAsnLysTyrArgLeuAlaAspLeuTyrArgTyrAspVa 539
 Db 120 CTACAGGCTTTAGTGCCCAATAGTACCGGCTTCAGATGATCTCTACCGATATGAT 179
 QY 539 LasThrGlnMetTrpThrIleLeuYsAspSerArgPheArgTyrLeuHisThrAl 559
 Db 180 GATACCCAGATGGACCATCTTAAGGACACCCGATTTTCGGTACTTCACACAGC 239
 QY 559 aValIleValSerGlyThrMetLeuValPheGlyGlyAsnThrHisAspThrSerWe 579
 Db 240 TGTGATAGTGGTGGACCACTGCTGGTGTGTTGGAGGAACACACACATGACATCAT 299
 QY 579 tSerHisGlyAlaLysCysPheSerSerAspPheMetAlaTyrAspIleAlaCysAspAr 599
 Db 300 GAGCATGGGCCCAATAGCTCTTCATGATTTTCATGGGCTATGACATGGCTGTGACCG 359
 QY 599 gTtpSerValLeu 603
 Db 360 CTGGTCAGTGCTT 372

RESULT 53
 CE522182
 LOCUS
 DEFINITION UI-M-GH0-cep-c-09-0-UI.r1 NIH_BMAP_GH0 Mus musculus cdna clone
 IMAGE:6842530 5', mRNA sequence.
 CE522182
 CE522182.1 GI:29355537
 EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NIH-MGC http://mgc.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cga08-remail.nih.gov
 Tissue Procurement: Dr. Jim Lin, University of Iowa
 cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
 DNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Distribution information can be found at
 http://genome.uiowa.edu/distribution/mousefl.html
 This clone was contributed by the Brain Molecular Anatomy Project
 (BMAP)

FEATURES

Location/Qualifiers
 1..758
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="CS7BL/6"
 /db_xref="taxon:10090"
 /clone="IMAGE:6842530"
 /tissue_type="Whole brain"
 /dev_stage="1, 5, and 15 days newborn"
 /lab_host="DH10B (T1 phage resistant)"
 /clone_lib="NIH BMAP_GH0"
 /note="Organ: Brain; Vector: pYX-Asc; Site_1: EcoR I;
 Site_2: Not I; The library was constructed according
 Bonaldi, Lennon and Soares, Genome Research, 5:791-806,
 1996. Denatured RNA was size fractionated on a 1% agarose
 gel. First strand cDNA synthesis was primed with oligo-dT
 primer containing a Not I site. Double strand cDNA was
 size selected according to mRNA size fraction, ligated
 with EcoR I adaptor, digested with NotI and then cloned
 directionally into pYX-Asc vector. The library tag
 sequence located between the Not I site and the PolyA tail
 is CCACTGAAT. This library was created for the University
 Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
 Developing Mouse Nervous System', supported by National
 Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
 program coordinator."

ORIGIN

Alignment Scores:
 Pred. No.: 1,78e-57 Length: 758
 Score: 84.00 Matches: 84
 Percent Similarity: 100.00% Conservatives: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 5.88% Indels: 0
 DB: 14 Gaps: 0
 US-09-787-097-12 (1-1429) x CB522182 (1-758)

QY 1346 GlyGlySerIleLysThrValProLysProIleAlaLeuLysProCysPheGlyAsnLys 1365
 Db 15 GGGGGAAGTATAAGACCGTTCCTTAAGCCCATTCCTGGAGCCCTTGTGTACAA 74
 QY 1366 AlaAlaValLeuSerValPheValArgLeuProArgGlyLeuGlyGlyLeuProPro 1385
 Db 75 GCGGAGTCTCTCTCTGTTATTCGTGAGGCTCCTCGAGAGCTGGGAGGATCCCTCTCT 134
 QY 1386 GlyGlnSerGlyLeuAlaValAlaSerAlaLeuValAspIleSerGlnMetProIle 1405
 Db 135 GGTCACTAGGTCTCGCTGTGCGCAGTCCCTGTGTGACATTTCTCAGCAGATGCCAATA 194
 QY 1406 ValTyrLysGlyLysSerGlyValAlaValArgAsnArgLysGlnGlnProAlaGlnPro 1425
 Db 195 GTGTACAGGAGAGTCTAGGAGCTGTAAAGAACCGGAACGAGCAGCGCGCTGCACAGCT 254
 QY 1426 GlyThrCysIle 1429
 Db 255 GGAACCTGCATT 266
 RESULT 54
 BU531905
 LOCUS
 DEFINITION AGENCOURT 10205588 NIH_MGC_126 Homo sapiens cdna clone
 IMAGE:6556819 5', mRNA sequence.
 BU531905
 BU531905.1 GI:22842346
 ACCESSION
 VERSION
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE
 1 (bases 1 to 778)
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/

```

/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UI-M-CG0p-brk-h-05-0-UI"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NIH_BMAP_Ret_S2"
/notes="Vector: p773D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; The
NIH BMAP Ret_S2 library is a subtracted library,
ultimately derived from mouse retina tissue libraries at
various stages of development. For a detailed description
of the library from which this clone was derived, please
visit our web site at brainest.eng.uiowa.edu. The tissue
for this library was contributed by Dr. Xin-Yuan Fu, Yale
University School of Medicine
TAG SEQ=None found"

```

ORIGIN

Alignment Scores:

Pred. No.:	3.17e-51	Length:	435
Score:	76.00	Matches:	76
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	5.32%	Indels:	0
DB:	12	Gaps:	0

US-09-787-097-12 (1-1429) X BI202684 (1-435)

123	GlyTrpValGlyGluGlnCysGlnHisCysGlyGlyArgPheArgLeuThrGlyGlySer	142
45	CGCTGGGTGGCGCAGCAATGCGACACTGGGGGGCGGCTTCAGACTAACTGGCTCTCT	104
143	GlyPheValThrAspGlyProGlyAsnTyrLysTyrLysThrLysCysThrTrpLeuLeu	162
105	GGATTGTGAACAGATGACCTGGGAATTATAAATATAAGACGAAGTGCACATGGCTCAATT	164
163	GluGlyGlnProAsnAArgIleMetArgLeuArgPheAsnHisPheAlaThrGluCysSer	182
165	GAAGGACAGCCAAATAGNATAATGAGACTTCGCTTCACCACTTTGCTACAGANGTAGC	224
183	TrpAspHisLeuTyrValTyrAspGlyAspSerIleTyrAlaProLeu	198
225	TGGACCATTTATGTTTATGATGGGCACTCAATCTACGCACCTCTG	272

RESULT 63

AW124828	488 bp	mRNA	linear	EST 22-OCT-1999
LOCUS	UI-M-BH2.1-apk-d-10-0-UI.s1	NIH BMAP M.S3.1	Mus musculus	cDNA clone
DEFINITION	UI-M-BH2.1-apk-d-10-0-UI 3'			mRNA sequence.
ACCESSION	AW124828			
VERSION	AW124828.1	GI:6100358		
KEYWORDS	EST.			
SOURCE	Mus musculus	(house mouse)		
ORGANISM	Mus musculus			
REFERENCE	Rukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
AUTHORS	1 (bases 1 to 488)			
AUTHORS	Bonaldo,M.F., Lennon,G. and Soares,M.B.			
TITLE	Normalization and subtraction: two approaches to facilitate gene discovery			
JOURNAL	Genome Res.	6 (9),	791-806	(1996)
MEDLINE	97044477			
PUBMED	8889548			
COMMENT	Contact: Chin, H			

Soares Lab Clone distribution: NIH BMAP cDNA clones will be made available by the means that is soon to be determined. When NIH determines the means for distribution of the BMAP cDNA clones, this record will be updated accordingly when that means is determined.

Seq primer: M13 Forward
POLYA=No.

FEATURES

source

1. 488
location/GenBank/1009090

```
/organism="Mus musculus"  
/mol_type="mRNA"  
/strain="C57BL/6J"  
/db_xref="taxon:100909"  
/clone="U1-M-BH2.1-ak-d-10-0-UI"  
/dev_stage="27-32 days"  
/lab_host="PHIBO (Life Technologies)"  
/clone_lib="NIH BMAP M S3.1"  
/note="Vector: pT7T3D-Pac (Pharmacia).  
polylinker; Site 1: Not I; Site 2: EcoRI.  
NIH BMAP M S3.1 library is a subtract  
series, ultimately derived from a mini-  
tagged normalized libraries from ten  
brain (cerebellum, brain stems, olfactory  
hypothalamus, cortex, amygdala, basal  
ganglia, striatum, hippocampus) after a  
subtractions to reduce the representation  
of which ESTs had already been generated.  
Serially subtracted libraries were generated  
process: NIH BMAP M S3.1, NIH BMAP M S3.1,  
the subtracted library (NIH BMAP M S3.1).  
as follows: PCR amplified cDNA insert  
clones from which 3' ESTs had been derived  
in the form of single-stranded circles  
single-stranded circles (subtracted 1  
by hydroxyapatite column chromatography  
double-stranded circles and electroporation  
bacteria (Life Technologies) to generate  
NIH BMAP M S3.1 library. This procedure  
previously described (Donaldo, Lennon  
Research 6:791-806, 1996)  
TAG_TISSUES=amygdala  
TAG_LIB=NIH_BMAP_M_S3.1  
TAG_SEQ=GTAG"
```

ORIGIN

Alignment scores.

Argument Scores:					
Pred. No.:	3.55e-51	Length:	488		
Score:	76.00	Matches:	76		
Percent Similarity:	100.00%	Conservative:	0		
Best local Similarity:	100.00%	Mismatches:	0		
Query Match:	5.32%	Indels:	0		
DB:	10	Gaps:	0		

US-09-787-097-12 (1-1429) X AW124828 (1-488)

123	GlyTrpValGlyGluInCysGlnHisCysGlyGlyArgPheArgLeuThrGlySerSer	142
44	GGCTGGGTGGCGCAGCAATGCCAGCACTGCGGGGCGCTTCAGACTAACTGGCTCTCT	103
143	GlyPheValThrAspGlyProGlyAsnTyrLysTyrLysThrLysCysThrTrpLeuLeu	162
104	GGATTGTAAACAGATGACCCTGGGAATTATAAATATAGACCAAGTGCATGGGTCTATT	163
163	GluGlyGlnProAsnArgIleMetArgLeuArgPheAsnHisPheAlaThrGluCysSer	182
164	GAAGACAGCCCAATAGNATATAGACCTTCGCTTCAACCACTTTGCTACAGATGTAGC	223
183	TrpAspHisLeuTyrValTyrAspGlyAspSerIleTyrAlaProLeu	198
224	TGGAGCACTTATATGTTTATGATGGGACTCAATCTACGCCACCTCTG	271

RESULT 64

REGUL 0-
BB952846